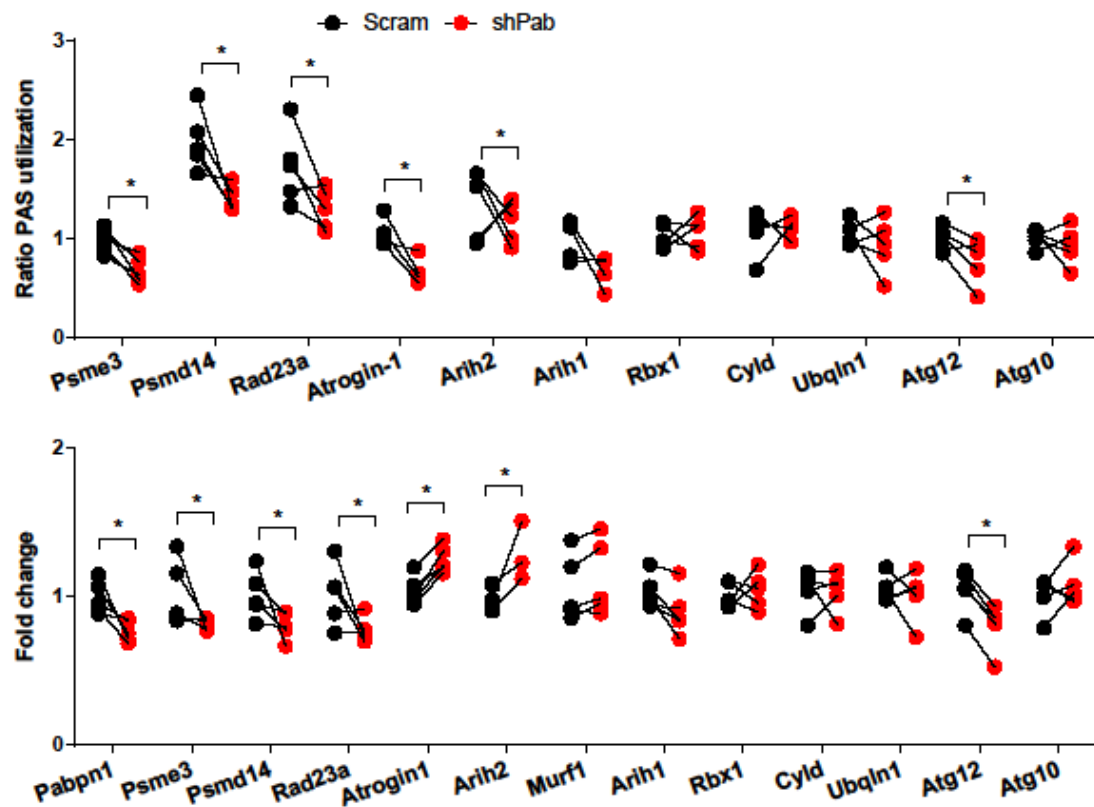


S1 Fig. Paired analysis of fold change and PAS utilization in five AAV9-injected mice.



A. PAS utilization is measured by the ratio of distal to total levels per gene. **B.** mRNA fold changes are calculated by normalizing to Hprt levels and to the Scram muscles. Statistical significance is assessed by a paired Student's t-test (*: $p < 0.05$).